Amendments to the Claims

This listing of the claims will replace all prior versions, and listings, of claims in this application.

Listing of Claims

1-7. **(Canceled)**

8. **(Currently Amended)** A method for identifying a subject who is a candidate for further diagnostic evaluation for a vascular disease or disorder comprising ~~the steps of:~~

~~a)~~ determining the identity of one or more of the nucleotides present at nucleotide positions selected from the group consisting of: 55322, 53502, 60793, and 58445, ~~52861, and/or 49556~~ of SEQ ID NO:1, ~~and/or the identity of the nucleotide present at nucleotide position 105290, 118019, and/or 89835 of SEQ ID NO:3,~~ or the full complement thereof~~; and~~

~~b) identifying the subject as a subject who is a candidate for further diagnostic evaluation for a vascular disease or disorder based on the identity of one or more of the nucleotides present at nucleotide positions 55322, 53502, 60793, and/or 58445, 52861, and/or 49556 of SEQ ID NO:1, and/or the identity of the nucleotide present at nucleotide position 105290, 118019, and/or 89835 of SEQ ID NO:3, or the complement thereof, or the full complement thereof~~, wherein the presence of at least one variant allele, or the full complement thereof, identifies the subject as a subject who is a candidate for further diagnostic evaluation for a vascular disease or disorder as compared with a subject having the reference allele at one or more of these positions.

9. **(Original)** The method of claim 8, wherein determining the identity of the nucleotides is by obtaining a nucleic acid sample from the subject.

10. **(Original)** The method of claim 8, wherein said further diagnostic evaluation consists of use of one or more vascular imaging devices.

11. **(Original)** The method of claim 10, wherein said vascular imaging device is selected from the group consisting of: angiography, cardiac ultrasound, coronary angiogram, magnetic resonance imagery, nuclear imaging, CT scan, myocardial perfusion imagery, electrocardiogram, and any combination thereof.

12. **(Original)** The method of claim 8, wherein further diagnostic evaluation is selected from the group consisting of: genetic analysis, familial health history analysis, lifestyle analysis, exercise stress tests, and any combination thereof.

13-40. **(Canceled)**

41. **(Currently Amended)** A method for diagnosing or aiding in the diagnosis of a vascular disease or disorder in a subject comprising determining the thrombospondin 1 (THBS1) genetic profile of the subject ~~The method of claim 40~~, wherein determining the subject's thrombospondin 1 (THBS1) ~~and/or THBS4~~ genetic profile comprises determining the identity of one or more of the nucleotides present at nucleotide positions selected from the group consisting of: 55322, 53502, 60793, and [[/or]] 58445[[,]] ~~52861, and/or 49556~~ of SEQ ID NO:1, ~~and/or the identity of the nucleotide present at nucleotide position 105290, 118019, and/or 89835 of SEQ ID NO:3,~~ or the full complement thereof [[,]]; wherein the presence of at least one variant allele, or the full complement thereof, is indicative of increased likelihood of a vascular disease or disorder in the subject as compared with a subject having the reference allele at one or more of these positions.

42. **(Currently Amended)** The method of claim [[40]] 41, further comprising utilizing a vascular imaging device to diagnose or aid in the diagnosis of a vascular disease or disorder.

43. **(Original)** The method of claim 42, wherein the vascular imaging device is selected from the group consisting of: angiography, cardiac ultrasound, coronary angiogram, magnetic resonance imagery, nuclear imaging, CT scan, myocardial perfusion imagery, electrocardiogram, and any combination thereof.

44-49. **(Canceled)**

50. **(Currently Amended)** The method of claim [[49]] 41, wherein determining the identity of the nucleotides is by obtaining a nucleic acid sample from the subject.

51. **(Currently Amended)** A method of diagnosing or aiding in the diagnosis of a vascular disease or disorder in a subject comprising determining the thrombospondin 1 (THBS1) genetic profile of the subject, wherein determining the subject's thrombospondin 1 (THBS1) genetic profile comprises determining the identity of one or more of the nucleotides present at nucleotide positions ~~the nucleotide at nucleotide position~~ 52861 [[and/]] or 49556 of SEQ ID NO:1, or the full complement thereof [[,]]; wherein the presence of at least one variant allele, or the full complement thereof, is indicative of decreased likelihood of a vascular disease or disorder in the subject as compared with a subject having the reference allele at one or more of these [[loci]] positions.

52. **(Original)** The method of claim 51, wherein determining the identity of the nucleotides is by obtaining a nucleic acid sample from the subject.

53. **(Currently Amended)** The method of claims [[49]] 41 or 51, wherein the vascular disease is selected from the group consisting of atherosclerosis, coronary artery disease, myocardial infarction, ischemia, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism.

54. **(Original)** The method of claim 53, wherein the vascular disease is myocardial infarction.

55. **(Original)** The method of claim 53, wherein the vascular disease is coronary artery disease.

56. **(Currently Amended)** A method for predicting the likelihood that a subject will have a vascular disease or disorder, comprising determining ~~the nucleotide at nucleotide position~~ the identity of one or more of the nucleotides present at nucleotide positions selected from the group consisting of: 55322, 53502, 60793, and [[/or]] 58445 of SEQ ID NO:1, ~~and/or the identity of the nucleotide present at nucleotide position 105290, 118019, and/or 89835 of SEQ ID NO:3,~~ or the full complement thereof,

wherein the presence of at least one variant allele, or the full complement[[s]] thereof, is indicative of increased likelihood of a vascular disease or disorder in the subject as compared with a subject having the reference allele at one or more of these [[loci]] positions.

57. **(Original)** The method of claim 56, wherein determining the identity of the nucleotides is by obtaining a nucleic acid sample from the subject.

58. **(Currently Amended)** A method for predicting the likelihood that a subject will have a vascular disease or disorder, comprising determining the identity of one or more of the nucleotides present at ~~nucleotide at~~ nucleotide positions 52861 [[and/]]or 49556 of SEQ ID NO:1, or the full complement thereof,

wherein the presence of at least one variant allele, or the full complement[[s]] thereof, is indicative of ~~increased~~ decreased likelihood of a vascular disease or disorder in the subject as compared with a subject having the reference allele at one or more of these [[loci]] positions.

59. **(Original)** The method of claim 58, wherein determining the identity of the nucleotides is by obtaining a nucleic acid sample from the subject.

60. **(Original)** The method of claim 56 or 58, wherein the vascular disease is selected from the group consisting of atherosclerosis, coronary artery disease, myocardial infarction, ischemia, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism.

61. **(Original)** The method of claim 60, wherein the vascular disease is myocardial infarction.

62. **(Original)** The method of claim 60, wherein the vascular disease is coronary artery disease.

63-134. **(Canceled)**

135. **(New)** A method for identifying a subject who is not a candidate for further diagnostic evaluation for a vascular disease or disorder comprising determining the identity of one or more of the nucleotides present at nucleotide positions 52861 or 49556 of SEQ ID NO:1, or the full complement thereof, wherein the presence of at least one variant allele, or the full complement thereof, identifies the subject as a subject who is not a candidate for further diagnostic evaluation for a vascular disease or disorder as compared with a subject having the reference allele at one or more of these positions.

136. **(New)** The method of any one of claims 8, 41, 51, 56, 58, or 135, wherein determining the identity of one or more nucleotides comprises contacting a sample nucleic acid from the subject with a probe or primers having sequences which are complementary to THBS1.

137. **(New)** The method of any one of claims 8, 41, 51, 56, 58, or 135, wherein determining the identity of one or more nucleotides comprises sequencing the nucleotide sequence.

138. **(New)** The method of any one of claims 8, 41, 51, 56, 58, or 135, wherein determining the identity of one or more nucleotides is carried out by restriction enzyme site analysis.

139. **(New)** The method of any one of claims 8, 41, 51, 56, 58, or 135, wherein determining the identity of one or more nucleotides is carried out by single-stranded conformation polymorphism (SSCP).

140. **(New)** The method of any one of claims 8, 41, 51, 56, 58, or 135, wherein determining the identity of one or more nucleotides is carried out by allele specific hybridization.

141. **(New)** The method of any one of claims 8, 41, 51, 56, 58, or 135, wherein determining the identity of one or more nucleotides is carried out by primer specific extension.

142. **(New)** The method of any one of claims 8, 41, 51, 56, 58, or 135, wherein determining the identity of one or more nucleotides is carried out by an oligonucleotide ligation assay (OLA).

143. **(New)** The method of any one of claims 8, 41, 51, 56, 58, or 135, wherein determining the identity of one or more nucleotides is carried out by denaturing high performance liquid chromatography (DHPLC).